\_\_\_\_\_\_

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=10; day=27; hr=6; min=59; sec=46; ms=23; ]

## Validated By CRFValidator v 1.0.3

Application No: 09514245 Version No: 1.0

Input Set:

Output Set:

**Started:** 2008-10-24 15:09:29.869

Finished: 2008-10-24 15:09:34.988

**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 119 ms

Total Warnings: 161

Total Errors: 9

No. of SeqIDs Defined: 170
Actual SeqID Count: 170

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## Input Set:

## Output Set:

**Started:** 2008-10-24 15:09:29.869

Finished: 2008-10-24 15:09:34.988

**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 119 ms

Total Warnings: 161

Total Errors: 9

No. of SeqIDs Defined: 170

356

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Actual SeqID Count: 170

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Organism is not permitted in <213> in SEQ ID (54)

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      BLANCHARD, Phillipe
     HUTET, Evelyne
     ARNAULD, Claire
      TRUONG, Catherine
     MAHE, Dominique
     CARIOLET, Roland
     MADEC, Francois
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Section   Sect								4		_		4	,		4	_	
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Second Price   Seco		_													_	_	210
Second Communication   Second Communication	O ± y		11011	DCI	DCI		110	O T y	var	СуБ		1110	C y B		Olu	1114	
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175	_					Ī		_			_	_				_	200
Glu	_	Pne		GTII	СТУ	GIU		vaı	Pne	ттр	Суз		ьeu	PIO	пта	Arg	
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225   230   235   236   235   236   246   247																	700
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gga atg gta ctc ctc aac tgc tgt ccc agc tgt aga agc tct cta tcg       864         Gly Met Val Leu Leu Asn Cys Cys Pro Ser Cys Arg Ser Ser Leu Ser 255       260       265         gag gat tac tac ttt gca att ttg gaa gac tgc tgg aga aca atc cac 912       260       265         Glu Asp Tyr Tyr Phe Ala Ile Leu Glu Asp Cys Trp Arg Thr Ile His 270       275       280         gga ggt acc cga agg ccg att tga agc agt gga ccc acc ctg tgc cct 960       295         Gly Gly Thr Arg Arg Pro Ile Ser Ser Gly Pro Thr Leu Cys Pro 285       290       295         ttt ccc ata taa aat aaa tta ctg agt ctt ttt tgt tat cac atc gta 1008       1008         Phe Pro Ile Asn Lys Leu Leu Ser Leu Phe Cys Tyr His Ile Val 300       305       310	ser	rne	ьие	σΤλ		GIN	ıуr	rne	Asp		GIN	ътп	ser	σΤΆ		rro	
Gly Met Val Leu Leu Asn Cys Cys Pro Ser Cys Arg Ser Ser Leu Ser 255																	0.64
gag gat tac tac ttt gca att ttg gaa gac tgc tgg aga aca atc cac       912         Glu Asp Tyr Tyr Phe Ala Ile Leu Glu Asp Cys Trp Arg Thr Ile His       270       275       280         gga ggt acc cga agg ccg att tga agc agt gga ccc acc ctg tgc cct       960         Gly Gly Thr Arg Arg Pro Ile       Ser Ser Gly Pro Thr Leu Cys Pro       295         ttt ccc ata taa aat taa aaa tta ctg agt ctt ttt tgt tat cac atc gta       1008         Phe Pro Ile       Asn Lys Leu Leu Ser Leu Phe Cys Tyr His Ile Val       300			_														864
gag gat tac tac ttt gca att ttg gaa gac tgc tgg aga aca atc cac 912 Glu Asp Tyr Tyr Phe Ala Ile Leu Glu Asp Cys Trp Arg Thr Ile His 270 275 280  gga ggt acc cga agg ccg att tga agc agt gga ccc acc ctg tgc cct 960 Gly Gly Thr Arg Arg Pro Ile Ser Ser Gly Pro Thr Leu Cys Pro 285 290 290  ttt ccc ata taa aat aaa tta ctg agt ctt ttt tgt tat cac atc gta 1008 Phe Pro Ile Asn Lys Leu Leu Ser Leu Phe Cys Tyr His Ile Val 300 305 310	GLy	Met	Val		Leu	Asn	Cys	Cys		Ser	Cys	Arg	Ser		Leu	Ser	
Glu Asp Tyr Tyr Phe Ala Ile Leu Glu Asp Cys Trp Arg Thr Ile His 270 280  gga ggt acc cga agg ccg att tga agc agt gga ccc acc ctg tgc cct 960  Gly Gly Thr Arg Arg Pro Ile Ser Ser Gly Pro Thr Leu Cys Pro 285 290 295  ttt ccc ata taa aat taa ctg agt ctt ttt tgt tat cac atc gta 1008  Phe Pro Ile Asn Lys Leu Leu Ser Leu Phe Cys Tyr His Ile Val 300 305 310				255					260					265			
gga ggt acc cga agg ccg att tga agc agt gga ccc acc ctg tgc cct 960 Gly Gly Thr Arg Arg Pro Ile Ser Ser Gly Pro Thr Leu Cys Pro 285 290 295  ttt ccc ata taa aat taa ctg agt ctt ttt tgt tat cac atc gta 1008 Phe Pro Ile Asn Lys Leu Leu Ser Leu Phe Cys Tyr His Ile Val 300 305 310																	912
gga ggt acc cga agg ccg att tga agc agt gga ccc acc ctg tgc cct 960  Gly Gly Thr Arg Arg Pro Ile Ser Ser Gly Pro Thr Leu Cys Pro 285 290 295  ttt ccc ata taa aat aaa tta ctg agt ctt ttt tgt tat cac atc gta 1008  Phe Pro Ile Asn Lys Leu Leu Ser Leu Phe Cys Tyr His Ile Val 300 305 310	Glu	Asp		Tyr	Phe	Ala	Ile		Glu	Asp	CA2	Trp		Thr	Ile	His	
Gly Gly Thr Arg Arg Pro Ile Ser Ser Gly Pro Thr Leu Cys Pro 285 290 295  ttt ccc ata taa aat aaa tta ctg agt ctt ttt tgt tat cac atc gta 1008  Phe Pro Ile Asn Lys Leu Leu Ser Leu Phe Cys Tyr His Ile Val 300 305 310			270					275					280				
285 290 295  ttt ccc ata taa aat aaa tta ctg agt ctt ttt tgt tat cac atc gta 1008  Phe Pro Ile Asn Lys Leu Leu Ser Leu Phe Cys Tyr His Ile Val  300 305 310	gga	ggt	acc	cga	agg	ccg	att	tga	agc	agt	gga	CCC	acc	ctg	tgc	cct	960
ttt ccc ata taa aat aaa tta ctg agt ctt ttt tgt tat cac atc gta 1008  Phe Pro Ile Asn Lys Leu Leu Ser Leu Phe Cys Tyr His Ile Val  300 305 310	Gly	Gly	Thr	Arg	Arg	Pro	Ile		Ser	Ser	Gly	Pro	Thr	Leu	Cys	Pro	
Phe Pro Ile Asn Lys Leu Leu Ser Leu Phe Cys Tyr His Ile Val 300 305 310		285					290						295				
300 305 310	ttt	CCC	ata	taa	aat	aaa	tta	ctg	agt	ctt	ttt	tgt	tat	cac	atc	gta	1008
	Phe	Pro	Ile		Asn	Lys	Leu	Leu	Ser	Leu	Phe	Cys	Tyr	His	Ile	Val	
atg gtt ttt att ttt att cat tta gag ggt ctt tca gga taa att ctc 1056		300						305					310				
	atg	gtt	ttt	att	ttt	att	cat	tta	gag	ggt	ctt	tca	gga	taa	att	ctc	1056

Met	Val 315	Phe	Ile	Phe	Ile	His 320	Leu	Glu	Gly	Leu	Ser 325	Gly		Ile	Leu	
tga	att	gta	cat	aaa	tag	tca	acc	tta	cca	cat	aat	ttt	ggg	ctg	tgg	1104
	Ile	Val	His	Lys		Ser	Thr	Leu	Pro	His	Asn	Phe	Gly	Leu	Trp	
		330						335					340			
ttg	cat	ttt	gga	gcg	cat	agc	cca	ggc	ctg	tgt	gct	cga	cat	tgg	tgt	1152
Leu	His	Phe	Gly	Ala	His	Ser		Gly	Leu	Cys	Ala	_	His	Trp	Суѕ	
		345					350					355				
		tta -													J J	1200
GLy	_	Leu	Asn	GLy	Ala		Ala	GLy	Phe	Phe	_	Tyr	Leu	Ala	GLy	
2 4 4	360	~ ~ ~	++~-	+++	or or <del>+</del>	365	~~+	a+ a	~- <del>-</del> +	+ ~~~	370	t or 5	- or <del>t</del>	2 4 4	+ 0.0	1040
		caa	_				_		_			_	<del>-</del>			1248
375	ASII	Gln	ьeu	rne	380	ьеи	Ala	ьeu	vai	385	СТУ		ser	Thr	тъ	
	aat	add	taa	agg		acc	tta	taa	tat		aaa	add	agt	agt	taa	1296
		Arg													caa	1270
390		9		9	1110	395	100	111			400		201	<b>~</b> C I		
	agg	ggt	cat	aqq	cca		taa	taa	aqq	aaa		caa	aqt	taa	cat	1344
		Gly														
	405					410					415					
cca	aga	taa	caa	cag	tgg	acc	caa	cac	ctc	ttt	gat	tag	agg	tga	tgg	1392
Pro	Arg		Gln	Gln	Trp	Thr	Gln	His	Leu	Phe	Asp		Arg		Trp	
420						425					430					
ggt	ctc	tgg	ggt	aaa	att	cat	att	tag	cct	ttc	taa	tac	ggt	agt	att	1440
Gly	Leu	Trp	Gly	Lys	Ile	His	Ile		Pro	Phe		Tyr	Gly	Ser	Ile	
		435					440							445		
gga	aag	gta	aaa	gta	aaa	ggt	tgg	tgc	cgc	ctg	agg	ggg	gga	gga	act	1488
Gly	Lys	Val		Val	Gly	Gly	Trp		Arg	Leu	Arg	Gly		Gly	Thr	
			450					455					460			<b></b>
		tgt	_			_	_				_		_			1536
GTÄ	Arg	Cys		TTE	Ser	Ата	Arg		$\mu$ $\tau$	$\sim \sim r$		10/100 T	/\ I 🗀	АТА	Ser	
at a	at a	465								SET	Lys	Met	AIA			
		$\alpha$ t $\alpha$	++=	+ ~~	t ~ a	~+ =	C 3 3	att	470		-			475	taa	159 <i>1</i>
		ctc Leu							470 ctc	tag	aaa	ggc	ggg	475 aat	tga	1584
var		ctc Leu	Leu						470 ctc Leu		aaa	ggc	ggg	475 aat	tga	1584
	Leu	Leu	Leu 480	Trp		Val	Gln	Ile	470 ctc Leu 485	tag	aaa Lys	ggc Gly	Gly	475 aat Asn		
aga	Leu tac		Leu 480 tct	Trp	ggc	Val gcc	Gln atc	Ile tgt	470 ctc Leu 485 aac	tag ggt	aaa Lys ttc	ggc Gly tga	ggg Gly agg	475 aat Asn	ggt	1584 1632
aga	Leu tac	Leu	Leu 480 tct	Trp	ggc	Val gcc	Gln atc	Ile tgt	470 ctc Leu 485 aac	tag ggt	aaa Lys ttc	ggc Gly tga	ggg Gly agg	475 aat Asn	ggt	
aga Arg 490	Leu tac Tyr	Leu	Leu 480 tct Ser	Trp ttc Phe	ggc Gly 495	Val gcc Ala	Gln atc Ile	Ile tgt Cys	470 ctc Leu 485 aac Asn	tag ggt Gly 500	aaa Lys ttc Phe	ggc Gly tga	ggg Gly agg Arg	475 aat Asn cgg Arg	ggt Gly	
aga Arg 490 gta	Leu tac Tyr	Leu ccg Pro	Leu 480 tct Ser	Trp ttc Phe gtc	ggc Gly 495 ttc	Val gcc Ala	Gln atc Ile gga	Ile tgt Cys gga	470 ctc Leu 485 aac Asn	tag ggt Gly 500 ttc	aaa Lys ttc Phe	ggc Gly tga gat	ggg Gly agg Arg	475 aat Asn cgg Arg	ggt Gly ggg	1632
aga Arg 490 gta	Leu tac Tyr	Leu ccg Pro	Leu 480 tct Ser	Trp ttc Phe gtc	ggc Gly 495 ttc	Val gcc Ala	Gln atc Ile gga	Ile tgt Cys gga	470 ctc Leu 485 aac Asn	tag ggt Gly 500 ttc	aaa Lys ttc Phe	ggc Gly tga gat	ggg Gly agg Arg	475 aat Asn cgg Arg	ggt Gly ggg	1632
aga Arg 490 gta Val 505	Leu tac Tyr cca Pro	Leu ccg Pro	Leu 480 tct Ser atg Met	Trp ttc Phe gtc Val	ggc Gly 495 ttc Phe 510	Val gcc Ala tcc Ser	Gln atc Ile gga Gly	lle tgt Cys gga Gly	470 ctc Leu 485 aac Asn tgt Cys	tag  ggt Gly 500 ttc Phe 515	aaa Lys ttc Phe caa Gln	ggc Gly tga gat Asp	ggg Gly agg Arg ggc Gly	475 aat Asn cgg Arg tgc Cys	ggt Gly ggg Gly 520	1632
aga Arg 490 gta Val 505 ggc	Leu tac Tyr cca Pro	Leu ccg Pro aat Asn	Leu 480 tct Ser atg Met	Trp  ttc Phe  gtc Val  ttc	ggc Gly 495 ttc Phe 510 tgc	Val gcc Ala tcc Ser	Gln atc Ile gga Gly aac	Ile tgt Cys gga Gly gcc	470 ctc Leu 485 aac Asn tgt Cys	tag  ggt Gly 500 ttc Phe 515 ttg	aaa Lys ttc Phe caa Gln	ggc Gly tga gat Asp	ggg Gly agg Arg ggc Gly	475 aat Asn cgg Arg tgc Cys	ggt Gly ggg Gly 520 tat	1632 1680
aga Arg 490 gta Val 505 ggc	Leu tac Tyr cca Pro	Leu ccg Pro aat Asn	Leu 480 tct Ser atg Met	Trp  ttc Phe  gtc Val  ttc	ggc Gly 495 ttc Phe 510 tgc	Val gcc Ala tcc Ser	Gln atc Ile gga Gly aac	Ile tgt Cys gga Gly gcc	470 ctc Leu 485 aac Asn tgt Cys	tag  ggt Gly 500 ttc Phe 515 ttg	aaa Lys ttc Phe caa Gln	ggc Gly tga gat Asp	ggg Gly agg Arg ggc Gly	475 aat Asn cgg Arg tgc Cys	ggt Gly ggg Gly 520 tat	1632 1680
aga Arg 490 gta Val 505 ggc Gly	Leu tac Tyr cca Pro ggg Gly	Leu ccg Pro aat Asn	Leu 480 tct Ser atg Met gtc Val	Trp  ttc Phe  gtc Val  ttc Phe 525	ggc Gly 495 ttc Phe 510 tgc Cys	Val gcc Ala tcc Ser ggt Gly	Gln atc Ile gga Gly aac Asn	Ile tgt Cys gga Gly gcc Ala	470 ctc Leu 485 aac Asn tgt Cys tcc Ser 530	tag  ggt Gly 500 ttc Phe 515 ttg Leu	aaa Lys ttc Phe caa Gln	ggc Gly tga gat Asp	ggg Gly agg Arg ggc Gly	475 aat Asn cgg Arg tgc Cys tcc Ser	ggt Gly ggg Gly 520 tat	1632 1680
aga Arg 490 gta Val 505 ggc Gly	tac Tyr cca Pro ggg Gly	Leu ccg Pro aat Asn tcc Ser	Leu 480 tct Ser atg Met yal aga Arg	Trp  ttc Phe  gtc Val  ttc Phe 525 agt	ggc Gly 495 ttc Phe 510 tgc Cys	Val gcc Ala tcc Ser ggt Gly ctg	atc Ile gga Gly aac Asn	Ile tgt Cys gga Gly gcc Ala	470 ctc Leu 485 aac Asn tgt Cys tcc Ser 530 tat Tyr	tag  ggt Gly 500 ttc Phe 515 ttg Leu	aaa Lys ttc Phe caa Gln	ggc Gly tga gat Asp	ggg Gly agg Arg ggc Gly	475 aat Asn cgg Arg tgc Cys tcc Ser	ggt Gly ggg Gly 520 tat	1632 1680 1728
aga Arg 490 gta Val 505 ggc Gly	tac Tyr cca Pro ggg Gly	Leu ccg Pro aat Asn tcc Ser	Leu 480 tct Ser atg Met yal aga	Trp  ttc Phe  gtc Val  ttc Phe 525 agt	ggc Gly 495 ttc Phe 510 tgc Cys	Val gcc Ala tcc Ser ggt Gly ctg	atc Ile gga Gly aac Asn	Ile tgt Cys gga Gly gcc Ala	470 ctc Leu 485 aac Asn tgt Cys tcc Ser 530 tat	tag  ggt Gly 500 ttc Phe 515 ttg Leu	aaa Lys ttc Phe caa Gln	ggc Gly tga gat Asp	ggg Gly agg Arg ggc Gly	475 aat Asn cgg Arg tgc Cys tcc Ser	ggt Gly ggg Gly 520 tat	1632 1680 1728
aga Arg 490 gta Val 505 ggc Gly aaa Lys	tac Tyr cca Pro ggg Gly	Leu ccg Pro aat Asn tcc Ser gaa Glu	Leu 480 tct Ser atg Met yal aga Arg	Trp  ttc Phe  gtc Val  ttc Phe 525 agt	ggc Gly 495 ttc Phe 510 tgc Cys	Val gcc Ala tcc Ser ggt Gly ctg	atc Ile gga Gly aac Asn	Ile tgt Cys gga Gly gcc Ala	470 ctc Leu 485 aac Asn tgt Cys tcc Ser 530 tat Tyr	tag  ggt Gly 500 ttc Phe 515 ttg Leu	aaa Lys ttc Phe caa Gln	ggc Gly tga gat Asp	ggg Gly agg Arg ggc Gly	475 aat Asn cgg Arg tgc Cys tcc Ser	ggt Gly ggg Gly 520 tat	1632 1680 1728

<210> SEQ ID NO 2 <211> LENGTH: 545 <212> TYPE: PRT

<213> ORGANISM: Type A PWD circovirus

<400> SEQUENCE: 2

4	Ser	Phe	Arg 35	Gly	Gly	Glu	Lys	Gln 40	Asn	Thr	Gly	Ala	Ser 45	Asn	Leu	Pro
I	Phe	Leu 50	Phe	Cys	Leu	Trp	Arg 55	Gly	Arg	Phe	Gly	Arg 60	Gly	Asn	Ser	Ser
	Pro 65	Pro	Gly	Val	Cys	Glu 70	Phe	Cys	Glu	Ala	Asp 75	Phe	Gln	Gly	Glu	Val 80
7	Val	Phe	Trp	Cys	Pro 85	Leu	Pro	His	Arg	Glu 90	Ser	Glu	Arg	Asn	Arg 95	Pro
Ž	Ala	Glu	Arg	Ile 100	Leu	Gln	Arg	Arg	Pro 105	His	Thr	Tyr	Arg	Val 110	Trp	Ser
4	Ser	Ala	Glu 115	Pro	Gly	Glu	Ala	Gln 120	Arg	Pro	Val	Tyr	Cys 125	Cys	Glu	Tyr
I	Pro	Phe 130	Gly	Asp	Gly	Val	Phe 135	Gly	Asp	Cys	Ser	Arg 140	Ala	Val	Ser	Cys
	Asn 145	Val	Cys	Glu	Lys	Phe 150	Pro	Arg	Ala	Gly	Thr 155	Phe	Glu	Ser	Glu	Arg 160
(	Glu	Asp	Ala	Glu	Ala 165	Leu	Glu	Asp	Ser	Cys 170	Thr	Arg	His	Ser	Gly 175	Pro
Ž	Ala	Arg	Leu	Trp 180	Glu	Glu	Pro	Val	Gly 185	Pro	Phe	Cys	Ala	Gly 190	His	Leu
-	Leu	Glu	Ala 195	Lys	Val	Val	Gly	Trp 200	Ile	Ser	Trp	Arg	Arg 205	Ser	Cys	Cys
I	Phe	Gly 210	Phe	Leu	Trp	Leu	Val 215	Thr	Leu	Gly	Ser	Thr 220	Glu	Thr	Val	Pro
	Val 225	Ser	Ile	Asp	Cys	Arg 230	Asp	Arg	Gly	Tyr	Cys 235	Ser	Phe	Phe	Gly	Pro 240
(	Gln	Tyr	Phe	Asp	Tyr 245	Gln	Gln	Ser	Gly	Pro 250	Pro	Gly	Met	Val	Leu 255	Leu
Ž	Asn	Cys	Cys	Pro 260	Ser	Cys	Arg	Ser	Ser 265	Leu	Ser	Glu	Asp	Tyr 270	Tyr	Phe
Ž	Ala	Ile	Leu 275	Glu	Asp	Cys	Trp	Arg 280	Thr	Ile	His	Gly	Gly 285	Thr	Arg	Arg
I	Pro	Ile 290	Ser	Ser	Gly	Pro	Thr 295	Leu	Cys	Pro	Phe	Pro 300	Ile	Asn	Lys	Leu
	Leu 305	Ser	Leu	Phe	Cys	Tyr 310	His	Ile	Val	Met	Val 315	Phe	Ile	Phe	Ile	His 320
-	Leu	Glu	Gly	Leu	Ser 325	Gly	Ile	Leu	Ile	Val 330	His	Lys	Ser	Thr	Leu 335	Pro
I	His	Asn	Phe	Gly 340	Leu	Trp	Leu	His	Phe 345	Gly	Ala	His	Ser	Pro 350	Gly	Leu
(	Cys	Ala	Arg 355	His	Trp	Cys	Gly	Tyr 360	Leu	Asn	Gly	Ala	Thr 365	Ala	Gly	Phe
I	Phe	Tyr 370	Tyr	Leu	Ala	Gly	Thr 375	Asn	Gln	Leu	Phe	Gly 380	Leu	Ala	Leu	Val
	Гrр 385	Gly	Ser	Thr	Trp	Ser 390	Gly	Arg	Arg	Ala	Ala 395	Leu	Trp	Cys	Gly	Gly 400
Ī	Arg	Ser	Ser	Tyr	Arg 405	Gly	His	Arg	Pro	Ser 410	Trp	Trp	Arg	Gly	Leu 415	Gln
4	Ser	Trp	His	Pro 420	Arg	Gln	Gln	Trp	Thr 425	Gln	His	Leu	Phe	Asp 430	Arg	Trp
(	Gly	Leu	Trp 435	Gly	Lys	Ile	His	11e 440	Pro	Phe	Tyr	Gly	Ser 445	Ile	Gly	Lys
7	Val	Gly 450	Val	Gly	Gly	Trp	Cys 455	Arg	Leu	Arg	Gly	Gly 460	Gly	Thr	Gly	Arg
(	Cys	Ile	Ser	Ala	Arg	His	Ser	Lys	Met	Ala	Ala	Ser	Val	Leu	Leu	Leu
4	465					470					475					480
-	Гrр	Val	Gln	Ile	Leu	Lys	Gly	Gly	Asn	Arg	Tyr	Pro	Ser	Phe	Gly	Ala

485 490 495 Ile Cys Asn Gly Phe Arg Arg Gly Val Pro Asn Met Val Phe Ser Gly 505 500 Gly Cys Phe Gln Asp Gly Cys Gly Gly Gly Ser Val Phe Cys Gly Asn 515 520 525 Ala Ser Leu Ala Thr Ser Ser Tyr Lys Ser Glu Arg Ser Ala Leu Leu 530 535 540 Tyr 545

<210> SEQ ID NO 3 <211> LENGTH: 577 <212> TYPE: PRT

<213> ORGANISM: Type A PWD circovirus

<400> SEQUENCE: 3

Gly Arg Thr Pro His Leu Gln Gly Phe Ala Asn Phe Ala Lys Lys Gln 65 70 75 80

Thr Phe Asn Lys Val Lys Trp Tyr Phe Gly Ala Arg Cys His Ile Glu
85 90 95

Lys Ala Lys Gly Thr Asp Gln Gln Asn Lys Glu Tyr Cys Ser Lys Glu
100 105 110

Gly His Ile Leu Ile Glu Cys Gly Ala Pro Arg Asn Gln Gly Lys Arg 115 120 125

Ser Asp Leu Ser Thr Ala Val Ser Thr Leu Leu Glu Thr Gly Ser Leu 130 135 140

Val Thr Val Ala Glu Gln Phe Pro Val Thr Tyr Val Arg Asn Phe Arg 145 150 150

Gly Leu Ala Glu Leu Leu Lys Val Ser Gly Lys Met Gln Lys Arg Asp 165 170 175

Trp Lys Thr Ala Val His Val Ile Val Gly Pro Pro Gly Cys Gly Lys

Ser Gln Trp Ala Arg Asn Phe Ala Glu Pro Arg Asp Thr Tyr Trp Lys
195 200 205

Pro Ser Arg Asn Lys Trp Trp Asp Gly Tyr His Gly Glu Glu Val Val 210 215 220

Val Leu Asp Asp Phe Tyr Gly Trp Leu Pro Trp Asp Asp Leu Leu Arg 225 230 240

Leu Cys Asp Arg Tyr Pro Leu Thr Val Glu Thr Lys Gly Gly Thr Val 255

Pro Phe Leu Ala Arg Ser Ile Leu Ile Thr Ser Asn Gln Ala Pro Gln 260 270

Glu Trp Tyr Ser Ser Thr Ala Val Pro Ala Val Glu Ala Leu Tyr Arg 275 280 285

Arg Ile Thr Thr Leu Gln Phe Trp Lys Thr Ala Gly Glu Gln Ser Thr 290 295 300

Glu Val Pro Glu Gly Arg Phe Glu Ala Val Asp Pro Pro Cys Ala Leu 305